

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 10/583,093A
Source: IFWP
Date Processed by STIC: 2/2/07

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 02/02/2007

PATENT APPLICATION: US/10/583,093A

TIME: 11:53:20

Input Set : A:\MERK3179.APP

Output Set: N:\CRF4\02022007\J583093A.raw

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3 <110> APPLICANT: FIEBIG, HELMUT
4     NANDY, ANDREAS
5     CROMWELL, OLIVER
7 <120> TITLE OF INVENTION: DNA SEQUENCE, AND RECOMBINANT PREPARATION OF THE GRASS
8     POLLEN ALLERGEN LOL P 4
10 <130> FILE REFERENCE: MERCK-3179
12 <140> CURRENT APPLICATION NUMBER: 10/583,093A
13 <141> CURRENT FILING DATE: 2006-06-15
15 <150> PRIOR APPLICATION NUMBER: PCT/EP04/013663
16 <151> PRIOR FILING DATE: 2004-12-01
18 <150> PRIOR APPLICATION NUMBER: DE 103 59 352.7
19 <151> PRIOR FILING DATE: 2003-12-16
21 <160> NUMBER OF SEQ ID NOS: 27
23 <170> SOFTWARE: PatentIn Ver. 3.3
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1272
27 <212> TYPE: DNA
28 <213> ORGANISM: Lolium perenne
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (2)..(1270)
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39 ggc ggg cac gac tac gag ggc ctc tcg tac cgc tcc ctg cag ccc gag 97
40 Gly Gly His Asp Tyr Glu Gly Leu Ser Tyr Arg Ser Leu Gln Pro Glu
41 20 25 30
43 aac ttc gca gtc gtc gac ctc aac cag atg cgg gcg gtg ttg gtg gac 145
44 Asn Phe Ala Val Val Asp Leu Asn Gln Met Arg Ala Val Leu Val Asp
45 35 40 45
47 ggt aag gcc cgc acg gcg tgg gtc gac tcc ggc gcg cag ctc ggc gag 193
48 Gly Lys Ala Arg Thr Ala Trp Val Asp Ser Gly Ala Gln Leu Gly Glu
49 50 55 60
51 ctc tac tac gcc atc tcc aag tat agc cgc acg ctg gcc ttc ccg gca 241
52 Leu Tyr Tyr Ala Ile Ser Lys Tyr Ser Arg Thr Leu Ala Phe Pro Ala
53 65 70 75 80
55 ggc gtt tgc ccg acc atc ggc gtg ggc ggc aac ctc gcg ggc ggc ggc 289
56 Gly Val Cys Pro Thr Ile Gly Val Gly Gly Asn Leu Ala Gly Gly Gly
57 85 90 95
59 ttc ggt atg ctg ctg cgc aag tac ggc atc gcc gca gag aac gtc atc 337
60 Phe Gly Met Leu Leu Arg Lys Tyr Gly Ile Ala Ala Glu Asn Val Ile
61 100 105 110

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63	gac	gtg	aag	ctc	gtc	gac	gcc	aac	ggc	aag	ctg	cac	gac	aag	aag	tcc	385
64	Asp	Val	Lys	Leu	Val	Asp	Ala	Asn	Gly	Lys	Leu	His	Asp	Lys	Lys	Ser	
65			115						120							125	
67	atg	ggc	gac	gac	cat	ttc	tgg	gcc	gtg	agg	ggt	ggc	ggc	ggc	gag	agc	433
68	Met	Gly	Asp	Asp	His	Phe	Trp	Ala	Val	Arg	Gly	Gly	Gly	Gly	Glu	Ser	
69			130						135							140	
71	ttc	ggc	atc	gtg	gtc	tcg	tgg	cag	gtg	aag	ctc	ctg	ccg	gtg	cct	ccc	481
72	Phe	Gly	Ile	Val	Val	Ser	Trp	Gln	Val	Lys	Leu	Leu	Pro	Val	Pro	Pro	
73	145								150							155	160
75	acg	gtg	acc	atc	ttc	aag	atc	ccc	aag	tca	gtc	agc	gag	ggc	gcc	gtg	529
76	Thr	Val	Thr	Ile	Phe	Lys	Ile	Pro	Lys	Ser	Val	Ser	Glu	Gly	Ala	Val	
77						165					170					175	
79	gac	atc	atc	aac	aag	tgg	caa	ctg	gtc	gcg	cct	caa	ctt	ccc	gcc	gac	577
80	Asp	Ile	Ile	Asn	Lys	Trp	Gln	Leu	Val	Ala	Pro	Gln	Leu	Pro	Ala	Asp	
81				180							185					190	
83	ctc	atg	atc	cgc	atc	att	gcg	atg	ggg	ccc	aag	gcc	acg	ttc	gag	gcc	625
84	Leu	Met	Ile	Arg	Ile	Ile	Ala	Met	Gly	Pro	Lys	Ala	Thr	Phe	Glu	Ala	
85				195							200					205	
87	atg	tac	ctc	ggc	acc	tgc	aaa	acc	ctg	acg	ccg	atg	atg	cag	agc	aag	673
88	Met	Tyr	Leu	Gly	Thr	Cys	Lys	Thr	Leu	Thr	Pro	Met	Met	Gln	Ser	Lys	
89				210							215					220	
91	ttc	ccc	gag	ctt	ggc	atg	aac	gcc	tcg	cac	tgc	aac	gag	atg	tca	tgg	721
92	Phe	Pro	Glu	Leu	Gly	Met	Asn	Ala	Ser	His	Cys	Asn	Glu	Met	Ser	Trp	
93	225								230							235	240
95	atc	gag	tcc	atc	ccc	ttc	gtc	cac	ctc	ggc	cat	agg	gat	tcc	ctg	gag	769
96	Ile	Glu	Ser	Ile	Pro	Phe	Val	His	Leu	Gly	His	Arg	Asp	Ser	Leu	Glu	
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99	ggc	gac	ctc	ctc	aac	cgg	aac	aac	acc	ttc	aag	ccc	ttt	gcg	gag	tac	817
100	Gly	Asp	Leu	Leu	Asn	Arg	Asn	Asn	Thr	Phe	Lys	Pro	Phe	Ala	Glu	Tyr	
101						260					265					270	
103	aaa	tcg	gac	tac	gtc	tac	gag	cca	ttc	ccc	aag	agc	gtg	tgg	gag	cag	865
104	Lys	Ser	Asp	Tyr	Val	Tyr	Glu	Pro	Phe	Pro	Lys	Ser	Val	Trp	Glu	Gln	
105				275							280					285	
107	atc	ttc	ggc	acc	tgg	ctc	gtg	aag	cct	ggt	gcg	ggg	att	atg	atc	ttt	913
108	Ile	Phe	Gly	Thr	Trp	Leu	Val	Lys	Pro	Gly	Ala	Gly	Ile	Met	Ile	Phe	
109				290							295					300	
111	gac	ccc	tac	ggt	gcc	acc	atc	agc	gct	acc	cca	gaa	gcg	gcg	acg	ccg	961
112	Asp	Pro	Tyr	Gly	Ala	Thr	Ile	Ser	Ala	Thr	Pro	Glu	Ala	Ala	Thr	Pro	
113	305						310					315				320	
115	ttc	cct	cac	cgc	aag	gga	gtc	ctc	ttc	aac	atc	cag	tac	gtc	aac	tac	1009
116	Phe	Pro	His	Arg	Lys	Gly	Val	Leu	Phe	Asn	Ile	Gln	Tyr	Val	Asn	Tyr	
117						325					330					335	
119	tgg	ttc	gct	ccg	gga	gcc	ggc	gcc	gcg	ccc	ttg	tca	tgg	agc	aag	gaa	1057
120	Trp	Phe	Ala	Pro	Gly	Ala	Gly	Ala	Ala	Pro	Leu	Ser	Trp	Ser	Lys	Glu	
121						340					345					350	
123	atc	tac	aac	tac	atg	gag	ccg	tac	gtg	agc	aag	aac	ccc	agg	cag	gcc	1105
124	Ile	Tyr	Asn	Tyr	Met	Glu	Pro	Tyr	Val	Ser	Lys	Asn	Pro	Arg	Gln	Ala	
125				355							360					365	
127	tac	gcc	aac	tac	agg	gac	atc	gac	ctc	ggg	agg	aac	gag	gtg	gtg	aat	1153

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132 Gly Val Ser Thr Tyr Ser Ser Gly Lys Val Trp Gly Gln Lys Tyr Phe
133 385      390      395      400
135 aag ggt aac ttc gag agg ctc gcc att acc aag ggc aag gtg gat cct 1249
136 Lys Gly Asn Phe Glu Arg Leu Ala Ile Thr Lys Gly Lys Val Asp Pro
137      405      410      415
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140 Thr Asp Tyr Phe Arg Asn Glu
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156 Asn Phe Ala Val Val Asp Leu Asn Gln Met Arg Ala Val Leu Val Asp
157      35      40      45
159 Gly Lys Ala Arg Thr Ala Trp Val Asp Ser Gly Ala Gln Leu Gly Glu
160      50      55      60
162 Leu Tyr Tyr Ala Ile Ser Lys Tyr Ser Arg Thr Leu Ala Phe Pro Ala
163 65      70      75      80
165 Gly Val Cys Pro Thr Ile Gly Val Gly Gly Asn Leu Ala Gly Gly Gly
166      85      90      95
168 Phe Gly Met Leu Leu Arg Lys Tyr Gly Ile Ala Ala Glu Asn Val Ile
169      100      105      110
171 Asp Val Lys Leu Val Asp Ala Asn Gly Lys Leu His Asp Lys Lys Ser
172      115      120      125
174 Met Gly Asp Asp His Phe Trp Ala Val Arg Gly Gly Gly Glu Ser
175      130      135      140
177 Phe Gly Ile Val Val Ser Trp Gln Val Lys Leu Leu Pro Val Pro Pro
178 145      150      155      160
180 Thr Val Thr Ile Phe Lys Ile Pro Lys Ser Val Ser Glu Gly Ala Val
181      165      170      175
183 Asp Ile Ile Asn Lys Trp Gln Leu Val Ala Pro Gln Leu Pro Ala Asp
184      180      185      190
186 Leu Met Ile Arg Ile Ile Ala Met Gly Pro Lys Ala Thr Phe Glu Ala
187      195      200      205
189 Met Tyr Leu Gly Thr Cys Lys Thr Leu Thr Pro Met Met Gln Ser Lys
190      210      215      220
192 Phe Pro Glu Leu Gly Met Asn Ala Ser His Cys Asn Glu Met Ser Trp
193 225      230      235      240
195 Ile Glu Ser Ile Pro Phe Val His Leu Gly His Arg Asp Ser Leu Glu
196      245      250      255
198 Gly Asp Leu Leu Asn Arg Asn Asn Thr Phe Lys Pro Phe Ala Glu Tyr

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199          260          265          270
201 Lys Ser Asp Tyr Val Tyr Glu Pro Phe Pro Lys Ser Val Trp Glu Gln
202          275          280          285
204 Ile Phe Gly Thr Trp Leu Val Lys Pro Gly Ala Gly Ile Met Ile Phe
205          290          295          300
207 Asp Pro Tyr Gly Ala Thr Ile Ser Ala Thr Pro Glu Ala Ala Thr Pro
208 305          310          315          320
210 Phe Pro His Arg Lys Gly Val Leu Phe Asn Ile Gln Tyr Val Asn Tyr
211          325          330          335
213 Trp Phe Ala Pro Gly Ala Gly Ala Ala Pro Leu Ser Trp Ser Lys Glu
214          340          345          350
216 Ile Tyr Asn Tyr Met Glu Pro Tyr Val Ser Lys Asn Pro Arg Gln Ala
217          355          360          365
219 Tyr Ala Asn Tyr Arg Asp Ile Asp Leu Gly Arg Asn Glu Val Val Asn
220          370          375          380
222 Gly Val Ser Thr Tyr Ser Ser Gly Lys Val Trp Gly Gln Lys Tyr Phe
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229          420
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234 <211> LENGTH: 1503
235 <212> TYPE: DNA
236 <213> ORGANISM: Lolium perenne
238 <220> FEATURE:
239 <221> NAME/KEY: CDS
240 <222> LOCATION: (1)..(1503)
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245 1 5 10 15
247 aaa gaa atc ccg ccg cgt ctg ttg tac gcg aaa tcg tcg ccg gcg tat 96
248 Lys Glu Ile Pro Pro Arg Leu Leu Tyr Ala Lys Ser Ser Pro Ala Tyr
249 20 25 30
251 ccc tca gtc ctg ggg cag acc atc cgg aac tcg agg tgg tcg tcg ccg 144
252 Pro Ser Val Leu Gly Gln Thr Ile Arg Asn Ser Arg Trp Ser Ser Pro
253 35 40 45
255 gac aac gtg aag ccg ctc tac atc atc acc ccc acc aac gtc tcc cac 192
256 Asp Asn Val Lys Pro Leu Tyr Ile Ile Thr Pro Thr Asn Val Ser His
257 50 55 60
259 atc cag tct gcc gtg gtg tgc ggc cgc cgt tac gac gtc cgc atc cgc 240
260 Ile Gln Ser Ala Val Val Cys Gly Arg Arg Tyr Asp Val Arg Ile Arg
261 65 70 75 80
263 gta cgc agc ggc ggg cac gac tac gag ggc ctc tcg tac cgc tcc ctg 288
264 Val Arg Ser Gly Gly His Asp Tyr Glu Gly Leu Ser Tyr Arg Ser Leu
265 85 90 95
267 cag ccc gag aac ttc gca gtc gtc gac ctc aac cag atg cgg gcg gtg 336
268 Gln Pro Glu Asn Phe Ala Val Val Asp Leu Asn Gln Met Arg Ala Val

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273			115				120	
275	ctc	ggc	gag	ctc	tac	tac	gcc	atc
276	Leu	Gly	Glu	Leu	Tyr	Tyr	Ala	Ile
277		130					135	
279	ttc	ccg	gca	ggc	gtt	tgc	ccg	acc
280	Phe	Pro	Ala	Gly	Val	Cys	Pro	Thr
281	145					150		155
283	ggc	ggc	ggc	ttc	ggt	atg	ctg	ctg
284	Gly	Gly	Gly	Phe	Gly	Met	Leu	Leu
285				165				170
287	aac	gtc	atc	gac	gtg	aag	ctc	gtc
288	Asn	Val	Ile	Asp	Val	Lys	Leu	Val
289			180					185
291	aag	aag	tcc	atg	ggc	gac	gac	cat
292	Lys	Lys	Ser	Met	Gly	Asp	Asp	His
293			195					200
295	ggc	gag	agc	ttc	ggc	atc	gtg	gtc
296	Gly	Glu	Ser	Phe	Gly	Ile	Val	Val
297		210					215	
299	gtg	cct	ccc	acg	gtg	acc	atc	ttc
300	Val	Pro	Pro	Thr	Val	Thr	Ile	Phe
301	225						230	
303	ggc	gcc	gtg	gac	atc	atc	aac	aag
304	Gly	Ala	Val	Asp	Ile	Ile	Asn	Lys
305				245				250
307	ccc	gcc	gac	ctc	atg	atc	cgc	atc
308	Pro	Ala	Asp	Leu	Met	Ile	Arg	Ile
309				260				265
311	ttc	gag	gcc	atg	tac	ctc	ggc	acc
312	Phe	Glu	Ala	Met	Tyr	Leu	Gly	Thr
313			275					280
315	cag	agc	aag	ttc	ccc	gag	ctt	ggc
316	Gln	Ser	Lys	Phe	Pro	Glu	Leu	Gly
317		290					295	
319	atg	tca	tgg	atc	gag	tcc	atc	ccc
320	Met	Ser	Trp	Ile	Glu	Ser	Ile	Pro
321	305						310	
323	tcc	ctg	gag	ggc	gac	ctc	ctc	aac
324	Ser	Leu	Glu	Gly	Asp	Leu	Leu	Asn
325				325				330
327	gcg	gag	tac	aaa	tgc	gac	tac	gtc
328	Ala	Glu	Tyr	Lys	Ser	Asp	Tyr	Val
329			340					345
331	tgg	gag	cag	atc	ttc	ggc	acc	tgg
332	Trp	Glu	Gln	Ile	Phe	Gly	Thr	Trp
333			355					360

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:17; Xaa Pos. 8

VERIFICATION SUMMARY

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L:777 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0